



Amelba

SEQUENCE LISTING

<110> Matsuzaki, Yumi
Kimura, Eiichiro
Nakamatsu, Tsuyoshi
Kurahashi, Osamu
Kawahara, Yoshio
Sugimoto, Shinichi

<120> Plasmid Autonomously Replicable in Coryneform Bacteria

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<140> US 09/636,458

<141> 2000-08-11

<150> JP 11-228391

<151> 1999-08-12

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<170> PatentIn version 3.1

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Arg Gly Trp Asn His Gln Asp Ala Ala Glu Phe Leu Ala His Leu Asp
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RECEIVED

OCT 31 2002

TECH CENTER 1600/2900

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Arg Ser Met Phe His Gly Cys Pro Thr Arg Asp Phe Ser Ala Ala Trp
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Gly Thr Arg Ser Leu Ser Arg Cys Gln Tyr Val Ala Leu Thr His Pro
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Gln Arg Ser Ala Val Leu Val Leu Asp Ile Asp Ile Pro Ser His Gln
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Ser Trp His Cys Gln His Asn Arg Val Asp Ile Leu Asp Glu Leu Met
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His Gln Glu Phe Ser Ser Gly Arg Ala Arg Ile Glu Ala Ala Arg Lys

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Lys Ala Leu Ala Thr Met Gly Arg Arg Gly Gly Gln Lys Ala Ala Glu
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Arg Leu Glu Ala Ala Asn Lys Arg Arg Gln Val Ser Trp Asn Lys Tyr
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Ala Ser Thr Asn Ser Gly Tyr Gly Phe Arg His Val Trp Ala Ser Leu
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Ser Trp His Cys Gln His Asn Arg Val Asp Ile Leu Asp Glu Leu Met
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His Gln Glu Phe Ser Ser Gly Arg Ala Arg Ile Glu Ala Ala Arg Lys
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Ala Thr Ala Glu Ala Lys Ala Leu Ala Ala Leu Asp Ala Thr Leu Pro
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Thr Ala Leu Glu Ala Ser Gly Asp Leu Ile Asp Gly Val Arg Val Leu
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Trp Ala Ala Glu Gly Arg Ala Ala Arg Asp Glu Thr Ala Phe Arg His
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Ala Leu Thr Val Gly Tyr Gln Leu Lys Ala Ala Gly Glu Arg Leu Lys
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Asp Ala Lys Ile Ile Asp Ala Tyr Glu Arg Ala Tyr Asn Val Ala Gln
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Pro Thr Val Ser Ala Arg Ser Thr Gln Thr Gln Ser Ser Arg Gly Arg
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Ala Ser Thr Asn Ser Gly Tyr Gly Phe Arg His Val Trp Ala Ser Leu
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Gln Arg Ser Ala Val Leu Val Leu Asp Ile Asp Ile Pro Ser His Gln
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His Gln Glu Phe Ser Ser Gly Arg Ala Arg Ile Glu Ala Ala Arg Lys
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Thr Ala Leu Glu Ala Ser Gly Asp Leu Ile Asp Gly Val Arg Val Leu
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Ala Leu Thr Val Gly Tyr Gln Leu Lys Ala Ala Gly Glu Arg Leu Lys
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Asp Ala Lys Ile Ile Asp Ala Tyr Glu Arg Ala Tyr Asn Val Ala Gln
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Lys Ala Leu Ala Thr Met Gly Arg Arg Gly Gly Gln Lys Ala Ala Glu
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 405 410 415

Arg Leu Glu Ala Ala Asn Lys Arg Arg Gln Val Ser Trp Asn Lys Tyr
 420 425 430

Ala Ser Thr Asn Ser Gly Tyr Gly Phe Arg His Val Trp Ala Ser Leu
 435 440 445

Glu Lys Cys Leu Arg Asp Glu Gln Ile Met Glu Glu Thr Gly Leu Ser
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Arg Ala Thr Val Thr Arg His Trp Val His Cys Glu Arg Leu Ala Cys
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Cys Gln Ile Leu Arg Gly Ala His Ala Val His Arg
 485 490

<210> 7
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 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
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Met Thr Leu Ala Asp Ser Pro Gly Thr Tyr Thr Ala Asp Ala Trp Asn	
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tac tcc aca gat ctg ttc gac acc cac cct gag ctg gct tta cgc tcc	96
Tyr Ser Thr Asp Leu Phe Asp Thr His Pro Glu Leu Ala Leu Arg Ser	
20 25 30	
egg ggt tgg aat cac cag gac gcc gcc gag ttc ctg gcc cac ctg gat	144
Arg Gly Trp Asn His Gln Asp Ala Ala Glu Phe Leu Ala His Leu Asp	
35 40 45	
cgc agc atg ttt cac ggg tgc ccc acc egg gat ttc tcc gcg gcc tgg	192
Arg Ser Met Phe His Gly Cys Pro Thr Arg Asp Phe Ser Ala Ala Trp	
50 55 60	

gtc aaa gac ccg gag acc gga gaa acc cgc cct aag ctg cac aga gtc Val Lys Asp Pro Glu Thr Gly Glu Thr Arg Pro Lys Leu His Arg Val 65 70 75 80	240
ggc acc cgg tgc ctt tcc cga tgc cag tac gtc gcg ctg acc cac ccg Gly Thr Arg Ser Leu Ser Arg Cys Gln Tyr Val Ala Leu Thr His Pro 85 90 95	288
cag cgc tcc gcg gtg ctg gtc tta gac atc gac atc ccc agc cac cag Gln Arg Ser Ala Val Leu Val Leu Asp Ile Asp Ile Pro Ser His Gln 100 105 110	336
gcc ggc ggg aac atc gag cac ctt cac ccg cag gtc tac gcc acc ttg Ala Gly Gly Asn Ile Glu His Leu His Pro Gln Val Tyr Ala Thr Leu 115 120 125	384
gag cgc tgg gca cgg gtg gag aaa gcg ccg gcc tgg atc ggg gtg aac Glu Arg Trp Ala Arg Val Glu Lys Ala Pro Ala Trp Ile Gly Val Asn 130 135 140	432
ccg ttg tca gga aag tgc cag ctc atc tgg tgc att gac ccg gtg ttc Pro Leu Ser Gly Lys Cys Gln Leu Ile Trp Cys Ile Asp Pro Val Phe 145 150 155 160	480
gcc gcc gag ggc acc acc agc ccg aac acc cgc ctg cta gcg gcc acc Ala Ala Glu Gly Thr Ser Pro Asn Thr Arg Leu Leu Ala Ala Thr 165 170 175	528
acc gag gaa atg acc cgt atg ttc ggc gct gac cag gca ttt tcc cac Thr Glu Glu Met Thr Arg Met Phe Gly Ala Asp Gln Ala Phe Ser His 180 185 190	576
cgg ctg agc cgg tgg ccg ctg cat gta tct gat gat ccg acc gcg tac Arg Leu Ser Arg Trp Pro Leu His Val Ser Asp Asp Pro Thr Ala Tyr 195 200 205	624
tcc tgg cac tgc cag cac aac cga gtc gat acg ctt gct gag ctg atg Ser Trp His Cys Gln His Asn Arg Val Asp Thr Leu Ala Glu Leu Met 210 215 220	672
gag gta gcc cgc acg atg acc gga tca aaa aag cca gat agc act gct Glu Val Ala Arg Thr Met Thr Gly Ser Lys Lys Pro Asp Ser Thr Ala 225 230 235 240	720
cac cag gag ttt tcc agc ggt cgg gca cgg atc gaa gcc gcg agg aaa His Gln Glu Phe Ser Ser Gly Arg Ala Arg Ile Glu Ala Ala Arg Lys 245 250 255	768
gcc acc gca gaa gcc aaa gcg ctt gct gcc tta gac gcc acg ctg cct Ala Thr Ala Glu Ala Lys Ala Leu Ala Ala Leu Asp Ala Thr Leu Pro 260 265 270	816
acg gcg ctg gag gca tca ggc gat ctc att gac ggg gtg cgg gtg ctg Thr Ala Leu Glu Ala Ser Gly Asp Leu Ile Asp Gly Val Arg Val Leu 275 280 285	864
tgg gca gca gag ggg cgt gca gcc cgt gat gag acg gcg ttt cgc cat	912

Trp	Ala	Ala	Glu	Gly	Arg	Ala	Ala	Arg	Asp	Glu	Thr	Ala	Phe	Arg	His		
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gcg	ttg	acc	gtg	ggg	tat	cag	ctt	aaa	gcc	gca	ggg	gaa	cgc	ctg	aaa	960	
Ala	Leu	Thr	Val	Gly	Tyr	Gln	Leu	Lys	Ala	Ala	Gly	Glu	Arg	Leu	Lys		
305					310				315						320		
gac	acc	aag	atc	att	gat	gcg	tat	gag	cgt	gcc	tac	aac	gtc	gcc	cag	1008	
Asp	Thr	Lys	Ile	Ile	Asp	Ala	Tyr	Glu	Arg	Ala	Tyr	Asn	Val	Ala	Gln		
			325					330						335			
gcg	gtg	ggg	gct	gat	ggg	cgt	gag	ccg	gat	ctg	cct	gcc	atg	cgt	gat	1056	
Ala	Val	Gly	Ala	Asp	Gly	Arg	Glu	Pro	Asp	Leu	Pro	Ala	Met	Arg	Asp		
			340					345					350				
cgt	cag	acg	ttg	gcc	cgt	cgt	gtg	cgc	gcc	tac	gtc	gct	aaa	ggc	cag	1104	
Arg	Gln	Thr	Leu	Ala	Arg	Arg	Val	Arg	Ala	Tyr	Val	Ala	Lys	Gly	Gln		
		355					360					365					
ccc	acg	gtg	agc	gcc	agg	agc	aca	cag	acc	cag	agc	agc	cgg	ggc	agg	1152	
Pro	Thr	Val	Ser	Ala	Arg	Ser	Thr	Gln	Thr	Gln	Ser	Ser	Arg	Gly	Arg		
		370				375					380						
aaa	gcc	ctg	gcc	acc	atg	gga	cgc	aga	ggc	gca	gcc	acc	tcg	aat	gca	1200	
Lys	Ala	Leu	Ala	Thr	Met	Gly	Arg	Arg	Gly	Ala	Ala	Thr	Ser	Asn	Ala		
385					390				395						400		
cgc	agg	tgg	gca	gac	cca	gaa	agc	gat	tac	gcc	cgc	caa	act	cgg	gag	1248	
Arg	Arg	Trp	Ala	Asp	Pro	Glu	Ser	Asp	Tyr	Ala	Arg	Gln	Thr	Arg	Glu		
				405				410						415			
cgt	tta	gcc	cga	gca	atg	agc	ttc	gta	cat	tca	gca	cag	acg	aga	aca	1296	
Arg	Leu	Ala	Arg	Ala	Met	Ser	Phe	Val	His	Ser	Ala	Gln	Thr	Arg	Thr		
			420					425					430				
agg	gcc	gga	tcc	tgg	cct	acg	ttt	ccg	agt	gca	agc	gcc	acg	gtt	acg	1344	
Arg	Ala	Gly	Ser	Trp	Pro	Thr	Phe	Pro	Ser	Ala	Ser	Ala	Thr	Val	Thr		
		435					440					445					
acc	cca	cga	gca	aag	aag	tcg	caa	cgg	agc	tag						1377	
Thr	Pro	Arg	Ala	Lys	Lys	Ser	Gln	Arg	Ser								
		450				455											

<210> 8
 <211> 458
 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 8

Met	Thr	Leu	Ala	Asp	Ser	Pro	Gly	Thr	Tyr	Thr	Ala	Asp	Ala	Trp	Asn
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Tyr	Ser	Thr	Asp	Leu	Phe	Asp	Thr	His	Pro	Glu	Leu	Ala	Leu	Arg	Ser
			20					25					30		

Arg Gly Trp Asn His Gln Asp Ala Ala Glu Phe Leu Ala His Leu Asp
 35 40 45

Arg Ser Met Phe His Gly Cys Pro Thr Arg Asp Phe Ser Ala Ala Trp
 50 55 60

Val Lys Asp Pro Glu Thr Gly Glu Thr Arg Pro Lys Leu His Arg Val
 65 70 75 80

Gly Thr Arg Ser Leu Ser Arg Cys Gln Tyr Val Ala Leu Thr His Pro
 85 90 95

Gln Arg Ser Ala Val Leu Val Leu Asp Ile Asp Ile Pro Ser His Gln
 100 105 110

Ala Gly Gly Asn Ile Glu His Leu His Pro Gln Val Tyr Ala Thr Leu
 115 120 125

Glu Arg Trp Ala Arg Val Glu Lys Ala Pro Ala Trp Ile Gly Val Asn
 130 135 140

Pro Leu Ser Gly Lys Cys Gln Leu Ile Trp Cys Ile Asp Pro Val Phe
 145 150 155 160

Ala Ala Glu Gly Thr Thr Ser Pro Asn Thr Arg Leu Leu Ala Ala Thr
 165 170 175

Thr Glu Glu Met Thr Arg Met Phe Gly Ala Asp Gln Ala Phe Ser His
 180 185 190

Arg Leu Ser Arg Trp Pro Leu His Val Ser Asp Asp Pro Thr Ala Tyr
 195 200 205

Ser Trp His Cys Gln His Asn Arg Val Asp Thr Leu Ala Glu Leu Met
 210 215 220

Glu Val Ala Arg Thr Met Thr Gly Ser Lys Lys Pro Asp Ser Thr Ala
 225 230 235 240

His Gln Glu Phe Ser Ser Gly Arg Ala Arg Ile Glu Ala Ala Arg Lys
 245 250 255

Ala Thr Ala Glu Ala Lys Ala Leu Ala Ala Leu Asp Ala Thr Leu Pro
260 265 270

Thr Ala Leu Glu Ala Ser Gly Asp Leu Ile Asp Gly Val Arg Val Leu
275 280 285

Trp Ala Ala Glu Gly Arg Ala Ala Arg Asp Glu Thr Ala Phe Arg His
290 295 300

Ala Leu Thr Val Gly Tyr Gln Leu Lys Ala Ala Gly Glu Arg Leu Lys
305 310 315 320

Asp Thr Lys Ile Ile Asp Ala Tyr Glu Arg Ala Tyr Asn Val Ala Gln
325 330 335

Ala Val Gly Ala Asp Gly Arg Glu Pro Asp Leu Pro Ala Met Arg Asp
340 345 350

Arg Gln Thr Leu Ala Arg Arg Val Arg Ala Tyr Val Ala Lys Gly Gln
355 360 365

Pro Thr Val Ser Ala Arg Ser Thr Gln Thr Gln Ser Ser Arg Gly Arg
370 375 380

Lys Ala Leu Ala Thr Met Gly Arg Arg Gly Ala Ala Thr Ser Asn Ala
385 390 395 400

Arg Arg Trp Ala Asp Pro Glu Ser Asp Tyr Ala Arg Gln Thr Arg Glu
405 410 415

Arg Leu Ala Arg Ala Met Ser Phe Val His Ser Ala Gln Thr Arg Thr
420 425 430

Arg Ala Gly Ser Trp Pro Thr Phe Pro Ser Ala Ser Ala Thr Val Thr
435 440 445

Thr Pro Arg Ala Lys Lys Ser Gln Arg Ser
450 455

<210> 9

<211> 4369

<212> DNA

<213> Corynebacterium thermoaminogenes

<220>
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 <222> (1)..(1476)
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 tac tcc act gat ctg ttc gac acc cac cct gag ctg gct tta cgc tcc 96
 Tyr Ser Thr Asp Leu Phe Asp Thr His Pro Glu Leu Ala Leu Arg Ser
 20 25 30
 cgg ggt tgg aat cac cag gac gcc gca gag ttc ctg gcc cac ctg gat 144
 Arg Gly Trp Asn His Gln Asp Ala Ala Glu Phe Leu Ala His Leu Asp
 35 40 45
 cgc agc atg ttt cac ggg tgc ccc acc cgg gat ttc tcc gcg gcc tgg 192
 Arg Ser Met Phe His Gly Cys Pro Thr Arg Asp Phe Ser Ala Ala Trp
 50 55 60
 gtc aaa gac ccg gaa acc gga gaa acc cgc ccc aag ctg cac aga gtt 240
 Val Lys Asp Pro Glu Thr Gly Glu Thr Arg Pro Lys Leu His Arg Val
 65 70 75 80
 ggc acc cgc tca ctt tcc cgg tgc cag tac gtt gcc ctg acc cac ccg 288
 Gly Thr Arg Ser Leu Ser Arg Cys Gln Tyr Val Ala Leu Thr His Pro
 85 90 95
 cag cgc tcc gcg gtg ctg gtc tta gac atc gac atc ccc agc cac cag 336
 Gln Arg Ser Ala Val Leu Val Leu Asp Ile Asp Ile Pro Ser His Gln
 100 105 110
 gcc ggc ggg aac atc gag cac ctt cac ccg cag gtg tac gcc acc ttg 384
 Ala Gly Gly Asn Ile Glu His Leu His Pro Gln Val Tyr Ala Thr Leu
 115 120 125
 gag cgt tgg gca cgg gtg gag aaa gcg ccg gcc tgg atc ggg gtg aac 432
 Glu Arg Trp Ala Arg Val Glu Lys Ala Pro Ala Trp Ile Gly Val Asn
 130 135 140
 ccg ttg tcg gga aag tgc cag ctc atc tgg tgc att gac ccg gtg ttc 480
 Pro Leu Ser Gly Lys Cys Gln Leu Ile Trp Cys Ile Asp Pro Val Phe
 145 150 155 160
 gcc gcc gag ggc acc acc agc tcg aac acc cgc ctg cta gcg gcc acc 528
 Ala Ala Glu Gly Thr Thr Ser Ser Asn Thr Arg Leu Leu Ala Ala Thr
 165 170 175
 acc gag gaa atg acc cgt gtg ttc ggc gct gac cag gca ttt tcc cac 576
 Thr Glu Glu Met Thr Arg Val Phe Gly Ala Asp Gln Ala Phe Ser His
 180 185 190
 cgg ctg agc cgg tgg ccg ctg cat gtt ttt gat gat ccg acc gcg tac 624

Arg	Leu	Ser	Arg	Trp	Pro	Leu	His	Val	Phe	Asp	Asp	Pro	Thr	Ala	Tyr		
	195						200					205					
tcc	tgg	cac	tgc	cag	cac	aac	cga	gtc	gat	att	ctt	gat	gag	ctg	atg	672	
Ser	Trp	His	Cys	Gln	His	Asn	Arg	Val	Asp	Ile	Leu	Asp	Glu	Leu	Met		
	210					215					220						
gag	gta	gcc	cgc	acg	atg	acc	gga	tca	aaa	aag	ccg	aga	aag	cac	gct	720	
Glu	Val	Ala	Arg	Thr	Met	Thr	Gly	Ser	Lys	Lys	Pro	Arg	Lys	His	Ala		
	225				230					235					240		
cac	cag	gag	ttt	tcc	agc	ggc	cgg	gca	cgg	atc	gaa	gcc	gcg	cgg	aaa	768	
His	Gln	Glu	Phe	Ser	Ser	Gly	Arg	Ala	Arg	Ile	Glu	Ala	Ala	Arg	Lys		
				245					250					255			
gcc	acc	gca	gag	gcc	aaa	gcg	ctt	gcc	gcc	ttg	gac	gcc	acg	ctg	cct	816	
Ala	Thr	Ala	Glu	Ala	Lys	Ala	Leu	Ala	Ala	Leu	Asp	Ala	Thr	Leu	Pro		
			260					265					270				
acg	gcg	ctg	gag	gca	tca	ggc	gat	ctc	att	gac	ggg	gtg	cgg	gtg	ttg	864	
Thr	Ala	Leu	Glu	Ala	Ser	Gly	Asp	Leu	Ile	Asp	Gly	Val	Arg	Val	Leu		
	275						280					285					
tgg	gca	gca	gag	ggg	cgt	gca	gcc	cgt	gat	gag	aca	gcg	ttt	cgc	cat	912	
Trp	Ala	Ala	Glu	Gly	Arg	Ala	Ala	Arg	Asp	Glu	Thr	Ala	Phe	Arg	His		
	290					295					300						
gcg	ttg	acc	gtg	ggc	tat	cag	ctt	aaa	gcc	gca	ggc	gaa	cgc	ctg	aaa	960	
Ala	Leu	Thr	Val	Gly	Tyr	Gln	Leu	Lys	Ala	Ala	Gly	Glu	Arg	Leu	Lys		
	305				310				315					320			
gat	gcc	aag	atc	att	gat	gcg	tat	gag	cgt	gcc	tac	aac	gtc	gcc	cag	1008	
Asp	Ala	Lys	Ile	Ile	Asp	Ala	Tyr	Glu	Arg	Ala	Tyr	Asn	Val	Ala	Gln		
				325					330					335			
gcg	gtg	gga	gct	gat	ggg	cgt	gaa	ccg	gat	ctg	cct	gcc	atg	cgt	gat	1056	
Ala	Val	Gly	Ala	Asp	Gly	Arg	Glu	Pro	Asp	Leu	Pro	Ala	Met	Arg	Asp		
			340					345					350				
cgt	cag	acg	atg	gcc	cgc	cgt	gtg	cgc	gcc	tac	gtc	gcc	aaa	ggc	cag	1104	
Arg	Gln	Thr	Met	Ala	Arg	Arg	Val	Arg	Ala	Tyr	Val	Ala	Lys	Gly	Gln		
		355					360					365					
ccc	acg	gtc	agc	gcc	agg	agc	aca	cag	acc	cag	agc	agt	cgg	ggc	cgg	1152	
Pro	Thr	Val	Ser	Ala	Arg	Ser	Thr	Gln	Thr	Gln	Ser	Ser	Arg	Gly	Arg		
		370				375						380					
aaa	gcc	ctg	gcc	acc	atg	ggc	cgc	aga	ggc	ggg	caa	aaa	gcc	gct	gaa	1200	
Lys	Ala	Leu	Ala	Thr	Met	Gly	Arg	Arg	Gly	Gly	Gln	Lys	Ala	Ala	Glu		
	385				390				395					400			
cgc	tgg	aaa	acc	gat	cct	aac	ggc	aaa	tac	gcc	caa	gaa	aac	cgc	caa	1248	
Arg	Trp	Lys	Thr	Asp	Pro	Asn	Gly	Lys	Tyr	Ala	Gln	Glu	Asn	Arg	Gln		
				405					410					415			
cga	ctc	gaa	gct	gca	aac	aag	cga	cgt	caa	gtc	agc	tgg	aac	aaa	tac	1296	
Arg	Leu	Glu	Ala	Ala	Asn	Lys	Arg	Arg	Gln	Val	Ser	Trp	Asn	Lys	Tyr		

420	425	430	
gcg agc acg aat tct ggc tac ggt ttc cga cac gta tgg gcc agc ttg			1344
Ala Ser Thr Asn Ser Gly Tyr Gly Phe Arg His Val Trp Ala Ser Leu			
435	440	445	
gaa aaa tgc cta cgc gac gag caa atc atg gaa gaa aca ggg ctt tca			1392
Glu Lys Cys Leu Arg Asp Glu Gln Ile Met Glu Glu Thr Gly Leu Ser			
450	455	460	
cga gct acc gtg acg cgc cat tgg gtg cac tgc gag agg ctg gcc tgc			1440
Arg Ala Thr Val Thr Arg His Trp Val His Cys Glu Arg Leu Ala Cys			
465	470	475	480
tgc caa atc ctt agg ggg gct cac gcc gta cac aga taacggttcc			1486
Cys Gln Ile Leu Arg Gly Ala His Ala Val His Arg			
485	490		
cacccccgtag gggtagcgct tgggtccctga agctccggct cccatccctc ctcagcactc			1546
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aaacgttatt	tatgaatctc	ttaggtgccg	cgcttgtagg	agcggtaatc	atggtcttga	4066
catggttatt	tattgatttt	gatgcacctg	gagcatggct	cggattcttt	attatcacca	4126
ccatcagtga	ttgctgcttt	agaagtcac	cacggacttt	gggaaaaacg	gcagggatct	4186
tccactgaca	atgattgata	aaacctgggt	gaacggaata	caaaacgcgc	aaaataacca	4246
ggcagttaaa	agaaaaacca	gataagctgc	accaatactt	gaaaaatgtt	gaacgccccg	4306
acagctgtaa	ctgtcgaggc	gtcggctaac	ccccagtcac	cagctgggag	aaagcactca	4366

aaa

4369

<210> 10
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<213> Corynebacterium thermoaminogenes

<400> 10

Met Thr Leu Ala Asp Ser Pro Gly Thr Tyr Thr Ala Asp Ala Trp Asn
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Tyr Ser Thr Asp Leu Phe Asp Thr His Pro Glu Leu Ala Leu Arg Ser
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Arg Gly Trp Asn His Gln Asp Ala Ala Glu Phe Leu Ala His Leu Asp
35 40 45

Arg Ser Met Phe His Gly Cys Pro Thr Arg Asp Phe Ser Ala Ala Trp
50 55 60

Val Lys Asp Pro Glu Thr Gly Glu Thr Arg Pro Lys Leu His Arg Val
65 70 75 80

Gly Thr Arg Ser Leu Ser Arg Cys Gln Tyr Val Ala Leu Thr His Pro
85 90 95

Gln Arg Ser Ala Val Leu Val Leu Asp Ile Asp Ile Pro Ser His Gln
100 105 110

Ala Gly Gly Asn Ile Glu His Leu His Pro Gln Val Tyr Ala Thr Leu
115 120 125

Glu Arg Trp Ala Arg Val Glu Lys Ala Pro Ala Trp Ile Gly Val Asn
130 135 140

Pro Leu Ser Gly Lys Cys Gln Leu Ile Trp Cys Ile Asp Pro Val Phe
145 150 155 160

Ala Ala Glu Gly Thr Thr Ser Ser Asn Thr Arg Leu Leu Ala Ala Thr
165 170 175

Thr Glu Glu Met Thr Arg Val Phe Gly Ala Asp Gln Ala Phe Ser His
180 185 190

Arg Leu Ser Arg Trp Pro Leu His Val Phe Asp Asp Pro Thr Ala Tyr
195 200 205

Ser Trp His Cys Gln His Asn Arg Val Asp Ile Leu Asp Glu Leu Met
210 215 220

Glu Val Ala Arg Thr Met Thr Gly Ser Lys Lys Pro Arg Lys His Ala
225 230 235 240

His Gln Glu Phe Ser Ser Gly Arg Ala Arg Ile Glu Ala Ala Arg Lys
245 250 255

Ala Thr Ala Glu Ala Lys Ala Leu Ala Ala Leu Asp Ala Thr Leu Pro
260 265 270

Thr Ala Leu Glu Ala Ser Gly Asp Leu Ile Asp Gly Val Arg Val Leu
275 280 285

Trp Ala Ala Glu Gly Arg Ala Ala Arg Asp Glu Thr Ala Phe Arg His
290 295 300

Ala Leu Thr Val Gly Tyr Gln Leu Lys Ala Ala Gly Glu Arg Leu Lys
305 310 315 320

Asp Ala Lys Ile Ile Asp Ala Tyr Glu Arg Ala Tyr Asn Val Ala Gln
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Ala Val Gly Ala Asp Gly Arg Glu Pro Asp Leu Pro Ala Met Arg Asp
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Arg Gln Thr Met Ala Arg Arg Val Arg Ala Tyr Val Ala Lys Gly Gln
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Pro Thr Val Ser Ala Arg Ser Thr Gln Thr Gln Ser Ser Arg Gly Arg
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Lys Ala Leu Ala Thr Met Gly Arg Arg Gly Gly Gln Lys Ala Ala Glu
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Arg Trp Lys Thr Asp Pro Asn Gly Lys Tyr Ala Gln Glu Asn Arg Gln
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Arg Leu Glu Ala Ala Asn Lys Arg Arg Gln Val Ser Trp Asn Lys Tyr
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Ala Ser Thr Asn Ser Gly Tyr Gly Phe Arg His Val Trp Ala Ser Leu
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Glu Lys Cys Leu Arg Asp Glu Gln Ile Met Glu Glu Thr Gly Leu Ser
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